

SEQUENCE LISTING

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<120> ICAM-4 BINDING SITES

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<160> 40

<170> PatentIn version 3.3

<210> 1

<211> 241

<212> PRT

<213> Homo sapiens

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Pro	Phe	Trp	Val	Arg	Met	Ser	Pro	Glu	Phe	Val	Ala	Val	Gln	Pro	Gly
			20					25					30		

Lys	Ser	Val	Gln	Leu	Asn	Cys	Ser	Asn	Ser	Cys	Pro	Gln	Pro	Gln	Asn
		35					40					45			

Ser	Ser	Leu	Arg	Thr	Pro	Leu	Arg	Gln	Gly	Lys	Thr	Leu	Arg	Gly	Pro
	50					55					60				

Gly	Trp	Val	Ser	Tyr	Gln	Leu	Leu	Asp	Val	Arg	Ala	Trp	Ser	Ser	Leu
65					70					75					80

Ala	His	Cys	Leu	Val	Thr	Cys	Ala	Gly	Lys	Thr	Arg	Trp	Ala	Thr	Ser
				85					90					95	

Arg	Ile	Thr	Ala	Tyr	Lys	Pro	Pro	His	Ser	Val	Ile	Leu	Glu	Pro	Pro
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Val	Leu	Lys	Gly	Arg	Lys	Tyr	Thr	Leu	Arg	Cys	His	Val	Thr	Gln	Val
		115					120					125			

2

Phe Pro Val Gly Tyr Leu Val Val Thr Leu Arg His Gly Ser Arg Val
130 135 140
Ile Tyr Ser Glu Ser Leu Glu Arg Phe Thr Gly Leu Asp Leu Ala Asn
145 150 155 160
Val Thr Leu Thr Tyr Glu Phe Ala Ala Gly Pro Arg Asp Phe Trp Gln
165 170 175
Pro Val Ile Cys His Ala Arg Leu Asn Leu Asp Gly Leu Val Val Arg
180 185 190
Asn Ser Ser Ala Pro Ile Thr Leu Met Leu Ala Trp Ser Pro Ala Pro
195 200 205
Thr Ala Leu Ala Ser Gly Ser Ile Ala Ala Leu Val Gly Ile Leu Leu
210 215 220
Thr Val Gly Ala Ala Tyr Leu Cys Lys Cys Leu Ala Met Lys Ser Gln
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 Gln Asn Ser Ser Leu Arg Thr Pro
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<210> 8
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<210> 9
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<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 9
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<210> 10
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<210> 11

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<213> Homo sapiens

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aacagctgtc	cccagccgca	gaattccagc	ctccgcaccc	cgctgcggca	aggcaagacg	180
ctcagagggc	cgggttgggt	gtcttaccag	ctgctcgacg	tgagggcctg	gagctccctc	240
gcgcactgcc	tcgtgacctg	cgcaggaaaa	acacgctggg	ccacctccag	gatcaccgcc	300
tacaaaccgc	cccacagcgt	gatttttgag	cctccgggtct	taaagggcag	gaaatacact	360
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<210> 15
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<400> 17
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oligonucleotide

<400> 18

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<210> 19

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<210> 20

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<210> 21

<211> 21

<212> DNA

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<210> 22

<211> 20

<212> DNA

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<210> 23
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<210> 24
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<210> 39
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<210> 40
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1				5					10					15		
ccc	ttc	tgg	gtg	cgc	atg	agc	ccg	gag	ttc	gtg	gct	gtg	cag	ccg	ggg	96
Pro	Phe	Trp	Val	Arg	Met	Ser	Pro	Glu	Phe	Val	Ala	Val	Gln	Pro	Gly	
			20					25					30			
aag	tca	gtg	cag	ctc	aat	tgc	agc	aac	agc	tgt	ccc	cag	ccg	cag	aat	144
Lys	Ser	Val	Gln	Leu	Asn	Cys	Ser	Asn	Ser	Cys	Pro	Gln	Pro	Gln	Asn	
		35					40				45					
tcc	agc	ctc	cgc	acc	ccg	ctg	cgg	caa	ggc	aag	acg	ctc	aga	ggg	ccg	192
Ser	Ser	Leu	Arg	Thr	Pro	Leu	Arg	Gln	Gly	Lys	Thr	Leu	Arg	Gly	Pro	
	50					55					60					
ggt	tgg	gtg	tct	tac	cag	ctg	ctc	gac	gtg	agg	gcc	tgg	agc	tcc	ctc	240
Gly	Trp	Val	Ser	Tyr	Gln	Leu	Leu	Asp	Val	Arg	Ala	Trp	Ser	Ser	Leu	
65					70				75						80	
gcg	cac	tgc	ctc	gtg	acc	tgc	gca	gga	aaa	aca	cgc	tgg	gcc	acc	tcc	288
Ala	His	Cys	Leu	Val	Thr	Cys	Ala	Gly	Lys	Thr	Arg	Trp	Ala	Thr	Ser	
			85						90					95		
agg	atc	acc	gcc	tac	aaa	ccg	ccc	cac	agc	gtg	att	ttg	gag	cct	ccg	336
Arg	Ile	Thr	Ala	Tyr	Lys	Pro	Pro	His	Ser	Val	Ile	Leu	Glu	Pro	Pro	
			100					105					110			
gtc	tta	aag	ggc	agg	aaa	tac	act	ttg	cgc	tgc	cac	gtg	acg	cag	gtg	384
Val	Leu	Lys	Gly	Arg	Lys	Tyr	Thr	Leu	Arg	Cys	His	Val	Thr	Gln	Val	
		115					120					125				
ttc	ccg	gtg	ggc	tac	ttg	gtg	gtg	acc	ctg	agg	cat	gga	agc	cgg	gtc	432
Phe	Pro	Val	Gly	Tyr	Leu	Val	Val	Thr	Leu	Arg	His	Gly	Ser	Arg	Val	
	130					135					140					
atc	tat	tcc	gaa	agc	ctg	gag	cgc	ttc	acc	ggc	ctg	gat	ctg	gcc	aac	480
Ile	Tyr	Ser	Glu	Ser	Leu	Glu	Arg	Phe	Thr	Gly	Leu	Asp	Leu	Ala	Asn	
145					150					155					160	
gtg	acc	ttg	acc	tac	gag	ttt	gct	gct	gga	ccc	cgc	gac	ttc	tgg	cag	528
Val	Thr	Leu	Thr	Tyr	Glu	Phe	Ala	Ala	Gly	Pro	Arg	Asp	Phe	Trp	Gln	
				165					170					175		
ccc	gtg	atc	tgc	cac	gcg	cgc	ctc	aat	ctc	gac	ggc	ctg	gtg	gtc	cgc	576
Pro	Val	Ile	Cys	His	Ala	Arg	Leu	Asn	Leu	Asp	Gly	Leu	Val	Val	Arg	
			180					185					190			
aac	agc	tcg	gca	ccc	att	aca	ctg	atg	ctc	gct	tgg	agc	ccc	gcg	ccc	624
Asn	Ser	Ser	Ala	Pro	Ile	Thr	Leu	Met	Leu	Ala	Trp	Ser	Pro	Ala	Pro	
		195					200					205				

aca	gct	ttg	gcc	tcc	ggg	tcc	atc	gct	gcc	ctt	gta	ggg	atc	ctc	ctc	672
Thr	Ala	Leu	Ala	Ser	Gly	Ser	Ile	Ala	Ala	Leu	Val	Gly	Ile	Leu	Leu	
210						215					220					
act	gtg	ggc	gct	gcg	tac	cta	tgc	aag	tgc	cta	gct	atg	aag	tcc	cag	720
Thr	Val	Gly	Ala	Ala	Tyr	Leu	Cys	Lys	Cys	Leu	Ala	Met	Lys	Ser	Gln	
225					230					235					240	
gcg																723
Ala																